

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 25, 2000, 20:27:11 ; Search time 90.74 seconds  
(without alignments)  
485.965 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDCKARKOPIKEEFTAEIH 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL12.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3384	100.0	636	4	015350 homo sapien
2	3304.5	97.7	637	6	Q9XSK8 cercopithec
3	2624	77.5	499	4	015351 homo sapien
4	2414.5	71.4	641	13	Q9W664 barbus barb
5	2379	70.3	497	11	Q9WUJ0 mus musculu
6	1789	52.9	680	11	088898 mus musculu
7	1786	52.8	641	4	075195 homo sapien
8	1777	52.5	634	11	035834 rattus norv
9	1743	51.5	586	11	089097 mus musculu
10	1727	51.0	596	4	075080 homo sapien
11	1397.5	38.3	448	4	076078 homo sapien
12	1384.5	38.0	483	11	088897 mus musculu
13	1248.5	36.9	393	4	075922 homo sapien
14	1238.5	36.6	389	11	088899 mus musculu
15	859.5	25.4	564	5	Q27937 loligo forb
16	821	24.3	369	13	Q9W678 barbus barb
17	789.5	23.3	376	13	Q93379 ictalurus p
18	750.5	22.2	378	12	P89002 mastomys na
19	750.5	22.2	391	11	Q9WUR6 cavia porce
20	736.5	21.8	391	6	036006 marmota mon

21	731.5	21.6	367	13	Q9W679 tetraodon m
22	724.5	21.4	393	4	Q16848 homo sapien
23	723.5	21.4	393	4	Q16811 homo sapien
24	720.5	21.3	393	4	Q15087 homo sapien
25	720.5	21.3	393	4	Q16535 homo sapien
26	720.5	21.3	393	4	Q16809 homo sapien
27	720	21.3	281	6	Q29475 canis famil
28	719.5	21.3	393	4	Q16808 homo sapien
29	718.5	21.2	393	4	Q15086 homo sapien
30	717.5	21.2	393	4	Q16810 homo sapien
31	716.5	21.2	265	13	Q9W682 oncorhynch
32	716.5	21.2	393	4	Q16807 homo sapien
33	715.5	21.1	390	11	070366 mus musculu
34	713.5	21.1	393	4	Q15088 homo sapien
35	712.5	21.1	265	13	Q9W681 oncorhynch
36	712.5	21.1	265	13	Q9W680 oncorhynch
37	686	20.3	342	13	057538 xiphophorus
38	686	20.3	342	13	092143 xiphophorus
39	685	20.1	285	6	Q95326 canis famil
40	680.5	20.1	286	12	P90332 mastomys na
41	671.5	19.8	286	12	P89003 mastomys na
42	639.5	18.9	238	12	P89004 mastomys na
43	576	17.0	205	11	035873 cricetus
44	573.5	16.9	196	6	Q29484 equus cabal
45	530.5	15.7	146	6	Q29469 canis famil

#### ALIGNMENTS

RESULT 1

015350 PRELIMINARY; PRT: 636 AA.  
 AC 015350;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE P53-LIKE TRANSCRIPTION FACTOR (P73 PROTEIN).  
 GN P73 OR TP73.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97433090.  
 RA KAGHAD M., BONNET H., YANG A., CREANCIER L., BISCAN J.C., VALENT A.,  
 RA MINTY A., CHALON P., LELIAS J.M., DUMONT X., FERRARA P., MCKEON F.,  
 RA CAPUT D.;  
 RT "Monoclonally expressed gene related to p53 at 1p36, a region  
 frequently deleted in neuroblastoma and other human cancers.";  
 RL Cell 90:809-819(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA YOSHIKAWA H., HAGIWARA K., HARRIS C.C.;  
 RT "Mutational analysis of p73 and p53 in Human Cancer Cell Lines.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MAI M., HUANG H., REED C., QIAN C., SMITH J.S., ALDERETE B.,  
 RA JENKINS R., SMITH D.I., LIU W.;  
 RT "Genomic organization and mutation analysis of p73 in  
 oligodendrogliomas with chromosome 1 p-arm deletions.";  
 RL Genomics 0:0-0(1998).  
 RN [4]  
 DR EMBL; Y11416; CAA72220.1;  
 DR EMBL; Y11416; CAA72221.1;  
 DR EMBL; AF077628; AAC61887.1;  
 DR EMBL; AF077616; AAC61887.1; JOINED.  
 DR EMBL; AF077617; AAC61887.1; JOINED.  
 DR EMBL; AF077618; AAC61887.1; JOINED.  
 DR EMBL; AF077619; AAC61887.1; JOINED.  
 DR EMBL; AF077620; AAC61887.1; JOINED.  
 DR EMBL; AF077621; AAC61887.1; JOINED.  
 DR EMBL; AF077622; AAC61887.1; JOINED.  
 DR EMBL; AF077624; AAC61887.1; JOINED.

EMBL: AF077625; AAC61887.1; JOINED.  
EMBL: AF077626; AAC61887.1; JOINED.  
EMBL: AF077627; AAC61887.1; JOINED.  
EMBL: AF079094; AAD39696.1; -  
EMBL: AF079083; AAD39696.1; JOINED.  
EMBL: AF079082; AAD39696.1; JOINED.  
EMBL: AF079084; AAD39696.1; JOINED.  
EMBL: AF079085; AAD39696.1; JOINED.  
EMBL: AF079086; AAD39696.1; JOINED.  
EMBL: AF079087; AAD39696.1; JOINED.  
EMBL: AF079088; AAD39696.1; JOINED.  
EMBL: AF079089; AAD39696.1; JOINED.  
EMBL: AF079090; AAD39696.1; JOINED.  
EMBL: AF079091; AAD39696.1; JOINED.  
EMBL: AF079092; AAD39696.1; JOINED.  
EMBL: AF079093; AAD39696.1; JOINED.  
HSP; P04637; IFSR.  
PFAM; PF00870; P53; 1.  
PRINTS; PR00386; P53SUPPRESSR.  
SEQUENCE 636 AA; C770F457 CRC32;

Query Match 100.0%; Score 3384; DB 4; Length 636;

Best Local Similarity 100.0%; Pred. No. 4.4e-263;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFLHGMNTS 60  
1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFLHGMNTS 60  
61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTHSPTAQPSSFTDMSAPVIPSNTD 120  
61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTHSPTAQPSSFTDMSAPVIPSNTD 120  
121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180  
121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180  
181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGRQSVVVPY 240  
181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGRQSVVVPY 240  
241 EPPQVGTFTTILYFNMCNNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300  
241 EPPQVGTFTTILYFNMCNNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300  
301 DRKADEHYREQALNESSAKNGAASKRAFQKSPAPVAPALGAGVKKRHGDEDTYYLQVR 360  
301 DRKADEHYREQALNESSAKNGAASKRAFQKSPAPVAPALGAGVKKRHGDEDTYYLQVR 360  
361 GRENFELMLKESLELMELVPOPLVDSYRQOQLLQRPSPHLOPPSYGVLSPMNKHVG 420  
361 GRENFELMLKESLELMELVPOPLVDSYRQOQLLQRPSPHLOPPSYGVLSPMNKHVG 420  
421 MNKLPSVNLQVGPQPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480  
421 MNKLPSVNLQVGPQPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480  
481 CTPPPPHADPSLVSLFTGLGCPNCEIYFTSGLOSIIHLQNTIETDLGALKIPEQYRMT 540  
481 CTPPPPHADPSLVSLFTGLGCPNCEIYFTSGLOSIIHLQNTIETDLGALKIPEQYRMT 540  
541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTITIPNR 600  
541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTITIPNR 600  
601 GPGGGPDENADFGDLPDCKARKQPIKEEFTAEI 636  
601 GPGGGPDENADFGDLPDCKARKQPIKEEFTAEI 636

RESULT 2  
9XSK8

ID O9XSK8 PRELIMINARY; PRT; 637 AA.  
AC O9XSK8;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DE 01-NOV-1999 (Tremblrel. 12, Last annotation update)  
DE P53-LIKE TRANSCRIPTION FACTOR.  
GN P73  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Cercopitheclidae; Cercopitheclinae;  
OC Chlorocebus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-KIDNEY;  
RA CAPUT D.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
FT EMBL; F11419; CAA72224.1; -. S -> -  
DR VARIANT 495 495  
SQ SEQUENCE 637 AA; 69630 MW; 8F092B51 CRC32;

Query Match 97.78; Score 3304.5; DB 6; Length 637;

Best Local Similarity 97.58; Pred. No. 1e-256;  
Matches 621; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFLHGMNTS 60  
Db 1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFLHGMNTS 60  
QY 61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTHSPTAQPSSFTDMSAPVIPSNTD 120  
Db 61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTHSPTAQPSSFTDMSAPVIPSNTD 120  
QY 121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180  
Db 121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180  
QY 181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGRQSVVVPY 240  
Db 181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGRQSVVVPY 240  
QY 241 EPPQVGTFTTILYFNMCNNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300  
Db 241 EPPQVGTFTTILYFNMCNNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300  
QY 301 DRKADEHYREQALNESSAKNGAASKRAFQKSPAPVAPALGAGVKKRHGDEDTYYLQVR 360  
Db 301 DRKADEHYREQALNESSAKNGAASKRAFQKSPAPVAPALGAGVKKRHGDEDTYYLQVR 360  
QY 361 GRENFELMLKESLELMELVPOPLVDSYRQOQLLQRPSPHLOPPSYGVLSPMNKHVG 420  
Db 361 GRENFELMLKESLELMELVPOPLVDSYRQOQLLQRPSPHLOPPSYGVLSPMNKHVG 420  
QY 421 MNKLPSVNLQVGPQPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480  
Db 421 MNKLPSVNLQVGPQPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480  
QY 481 CTPPPPHADPSLVSLFTGLGCPNCEIYFTSGLOSIIHLQNTIETDLGALKIPEQYRMT 540  
Db 481 CTPPPPHADPSLVSLFTGLGCPNCEIYFTSGLOSIIHLQNTIETDLGALKIPEQYRMT 540  
QY 541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTITIPNR 599  
Db 541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTITIPNR 599  
QY 600 GPGGGPDENADFGDLPDCKARKQPIKEEFTAEI 636  
Db 600 GPGGGPDENADFGDLPDCKARKQPIKEEFTAEI 637

RESULT 3  
OL5351  
ID OL5351 PRELIMINARY; PRT; 499 AA.



Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
[1]  
SEQUENCE FROM N.A.  
STRAIN-D3 (129SV);  
MEDLINE; 99247549.  
HERRANZ M., SANTOS J., SALIDO E., FERNANDEZ-PIQUERAS J., SERRANO M.;  
"Mouse p73 gene maps to the distal part of chromosome 4 and might be  
involved in the progression of gamma-radiation-induced T-cell  
lymphomas";  
Cancer Res. 59:2068-2071(1999).  
EMBL; AF138873; AA032213.1; -;  
NON\_TER 1  
SEQUENCE 497 AA; 54717 MW; FFD43964 CRC32;

Query Match 70.38; Score 2379; DB 11; Length 497;  
Best Local Similarity 90.28; Pred. No. 1.1e-182;  
Matches 450; Conservative 19; Mismatches 22; Indels 8; Gaps 5;  
144 YSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHVTDVWRCNHELGRDF 203  
1 YSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHVTDVWRCNHELGRDF 60  
204 NEGQAPASHLIRVEGNLSYDDPTGQSVVYPPVPGVGTETITLYNFMCSNV 263  
61 NEGQAPASHLIRVEGNLSYDDPTGQSVVYPPVPGVGTETITLYNFMCSNV 120  
264 GCMNRRPILITILEMRDQVLRSGRSEGRICACPGDRKADDEHYREQALNESAKNG 323  
121 GCMNRRPILITILEMRDQVLRSGRSEGRICACPGDRKADDEHYREQALNESAKNG 180  
324 AASKRAFPQSPNAPALGAGVKKRHGDETYLQV-RGRENFEILMKLESLELMELVP 382  
181 AASKRAFPQSPNAPALGAGVKKRHGDETYLQV-RGRENFEILMKLESLELMELVP 240  
383 OPLVDYSR--QQQLLQRPSPYSGVLPSPNPKVHGGMNKLPSVNLQVGPSPHSA 440  
241 OHLVDYSRQQQLLQRPSPYSGVLPSPNPKVHGGMNKLPSVNLQVGPSPHSA 300  
441 ATPNLGVPVGMNHNHGVANGEMSSSSASQSVSGSHCTPPPYHADPSLVFLTGL 500  
301 AGPNLGMGSLNASHGSPANGEMNGHSSQTMVSGSHCTPPPYHADPSLVFLTGL 360  
501 GPCNCEIYFTSGQSIYHLQNTIEDLGALKIPEQYRMTIWRGLQDLKOGHDYSTAOL 560  
361 GPCNCEIYFTSGQSIYHLQNTIEDLGALKIPEQYRMTIWRGLQDLKOGHDYSTAOL 418  
561 LR-SNNAATISIGSGELQQRVMEAVHFRVHTITIPNRRGPGG--GPDWADFGDLP 617  
419 LRSSNNAATISIGSGELQQRVMEAVHFRVHTITIPNRRGPGGAGVTPDWDADFGDLP 478  
618 DCKARKQPIKEEFTETESH 636  
479 DCKARKQPIKEEFTETESH 497

SULT 6  
8898  
O8898 PRELIMINARY; PRT; 580 AA.  
O8898;  
01-NOV-1998 (TRENBLrel. 08, Created)  
01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
01-NOV-1999 (TRENBLrel. 12, Last annotation update)  
TA\*P63 ALPHA  
Mus musculus (Mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
[1]  
SEQUENCE FROM N.A.  
MEDLINE; 98448095.  
YANG A., KAGHAD M., GILLET E., FLEMING M.D., DOTSCH V., ANDREWS N.C.,  
CAPUT D., MCKEON F.;  
"p53, a p53 homolog at 3q27-29, encodes multiple products with

transactivating, death-inducing, and dominant-negative activities";  
Mol. Cell 2:303-316(1998).  
DR EMBL; AF075436; AAC62641.1; -;  
DR HSP; P04637; LYCS.  
DR PFAM; PF00870; P53; 1.  
DR PRINTS; PRO0386; P53SUPPRESSR.  
SQ SEQUENCE 680 AA; 76788 MW; 230EDIFA CRC32;

Query Match 52.9%; Score 1789; DB 11; Length 680;  
Best Local Similarity 55.1%; Pred. No. 3e-135;  
Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps 18;  
QY 1 MAQSTAT---SPDGTTEHLWSSLEP-----DSTYFDLPSSRGNNVVGTTSS 48  
DB 40 MSSTSTSTSELSPE---VFQHWDFLEQPSVQVFIENFVDESENGATNKI----EIS 92  
QY 49 MDVFLHLEGMTS-----VMAQNLSSLSTMDQSSRAASASPTPEHAA-SVPTSPYAPQ 102  
DB 93 MDCIRMQSDSLSDPMWPQYTNLGLNSMDQQTQNGSSSTSPYNDHAQNSVTAPSPYAPQ 152  
QY 103 SSTFEDTSPAPVTPSNTDYPGPHFEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQ 162  
DB 153 SSTFEDTSPAPVTPSNTDYPGPHFEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQ 212  
QY 163 IKYSTPPPGTAIRAMPVYKKAHVTDVWRCNHELGRDFNEGQAPASHLIRVEGNL 222  
DB 213 IKYSTPPPGTAIRAMPVYKKAHVTDVWRCNHELGRDFNEGQAPASHLIRVEGNL 272  
QY 223 SQVDDPVTGROSVVYPPVPGVGTETITLYNFMCSNVGGMNRRPILITILEMRD 282  
DB 273 AQVDEPTITGROSVVYPPVPGVGTETITLYNFMCSNVGGMNRRPILITILEMRD 332  
QY 283 QVLRSGRSEGRICACPGDRKADDEHYREQALNESAKNGAASKRAFPQSPNAPALGA 342  
DB 333 QVLRSGRSEGRICACPGDRKADDEHYREQALNESAKNGAASKRAFPQSPNAPALGA 388  
QY 343 GVKRRHGDETYLQV-RGRENFEILMKLESLELMELVPDPSLVFLTGL 397  
DB 389 SIKRRSPDELLYLPVGRGTYEMLKLESLELMELVPDPSLVFLTGL 448  
QY 398 RPSHL-PPSYGVLSPNPKVHGGMNKLPSVNLQVGPSPHSAATNLGVPVGP---M 452  
DB 449 KQTSMSQSSYNSPPLNKN-SNKLPSVQLIN--PQORNALPTTMEGANGNIPM 505  
QY 453 LNNHGVANGEMSSSSASQSVSGSHCTPPPYHADPSLVFLTGLGCPNCI 506  
DB 506 MGTH---MPMAGDMGLSPTQALPPPLSNPSTSHCTPPPYPTDCSIVSFLARLGCSSL 562  
QY 507 EYFTSGLOSIYHLQNTIEDLGALKIPEQYRMTIWRGLQDLKOGHDYSTAOL 565  
DB 563 DIFTTQGLTITTYIEHYSMDLALUKIPEQYRMTIWRGLQDLKOGHDYSTAOL 622  
QY 566 AATISIGSGELQQRVMEAVHFRVHTITIPNRRGPGGAGVTPDWDADFGDLP 625  
DB 623 ASTVSV-GSSETRGERVIDAVRFTLRQTISFPFR-----DENNDNFDMDSRNRKQR 674  
QY 626 IKEE 629  
DB 675 IKEE 678

RESULT 7  
O75195 PRELIMINARY; PRT; 641 AA.  
ID O75195  
AC O75195;  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)  
DE P51B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.

[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE-SKELETAL MUSCLE;  
RX MEDLINE; 98324755.  
RA OSADA M., OHBA M., KAWAHARA C., ISHIKAWA R., KATOH I.,  
RA IKAWA Y., NIMURA Y., NAKAGAWARA A., OGINATA M.,  
RT "Cloning and functional analysis of human p51, which structurally and  
RT functionally resembles p53."  
RL Nat. Med. 4:839-844(1998).  
DR EMBL; AB016073; BAA32593.1; -.  
DR HSP; P04637; 1YCS.  
DR PFAM; PFO0870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
SQ SEQUENCE 641 AA; 72019 MW; 2818F74C CRC32;

Query Match 52.8%; Score 1786; DB 4; Length 641;  
Best Local Similarity 55.0%; Pred. No. 4.8e-135;  
Matches 365; Conservative 94; Mismatches 145; Indels 60; Gaps 18;

QY 1 MAOSTAT-----SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNVVGTTSS 48  
DB 1 MSSTQTNELSP-----VFGHWDLEQICSVQPIDLNFVDEPSEDGATNKI-----EIS 53  
QY 49 MDVHLEGMTS-----VMAQFNLLSTMDQSSRAASAPYTPHAA-SVTPHSPYAP 102  
DB 54 MDCIRMDSDLSDPMPQYTNLGLLNMDOQIQNGSSSTPYNTDHAQNSVAPSPYAP 113  
QY 103 SSTFDMSAPVPSNTDYPGPHFEVTFQOSSTAKSATWYSPLLKLYCOIATCPIQ 162  
DB 114 SSTFDALSPSPALPSNTDYPGPHSFVDFQOSSTAKSATWYSTELKLYCOIATCPIQ 173  
QY 163 IKVSTPPPGTAIRAMPVYKAEHVDVVKRCNPNHSLGRDFNEGOSAPASHLIRVEGNL 222  
DB 174 IKVTPPQGAIRAMPVYKAEHVEVVKRCNPNHSLREFNEGQIAPPASHLIRVEGNH 233  
QY 223 SQYVDDPVTRGQSVVYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDG 282  
DB 234 AQVDEPITGRQSVLYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDG 293  
QY 283 QVLRGRSFEGRICACGRDKADEHYREQQALNESSAKRAKQSPVAPALGA 342  
DB 294 QVLRGRCFEGRICACGRDKADEHSIRKQV--SDSTANGDGTFRPQNTHTGQM--T 349  
QY 343 GVKRRHGEDTYLVQVRENFELMKLESLELMELVQPLVDVSYRQOQO-----LLQ 397  
DB 350 SIKRRSPDDELLYLVQVRENYEMLLKIKESLELMQYLPQHTIETIRQOQOQHLLQ 409  
QY 398 RPSHLQ-PPSYGVLSPMKNVHGMMKLPVNLQYQPPHSSAATNLGPVGPQ---M 452  
DB 410 KQTSISPSYGNSSPPLKNN--SMKLPVSQLIN--PQNNALTPPTPDGMGANTPM 466  
QY 453 LNNHGHAVPANGEMSSSSSAQ-----SMVSGSHCTPPPPYHADPSLYSLTGLGCPNCI 506  
DB 467 MGTN--MPMAGDMGLSPTQALPPPLSPSTSHCTPPPPYPTDCSIVGFLARLGCSSCL 523  
QY 507 EYTSQGLQSIYHLQNTLEDIGALKIPEQYRMTWRGLQDLKQGHYSTAQQLRS--SN 565  
DB 524 DYFTTGLTIVQIHYSDMLASLKIPEQFRHAIWKGLDRLHQLRHEFSFSSHLRLTPSS 583  
QY 566 AATISIGGSELQQRQVMEAVHFRVHTITIPNRGPGGPPDEWADFGLDPCCKARKQ 625  
DB 584 ASIVSV-GSSETRGERVIDAVRFTLRQITISFPFR-----DEWDFNDFMDARRNQOR 635  
QY 626 IKKE 629  
DB 636 IKKE 639

RESULT 8  
O35834  
ID O35834 PRELIMINARY; PRT; 634 AA.  
AC O35834;

DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE KET PROTEIN (FRAGMENT).  
GN KET.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-LINGUAL EPITHELIUM;  
RX MEDLINE; 97460723.  
RA SCHWALE H., BAMBERGER C.;  
RT "A novel protein with strong homology to the tumor suppressor p53."  
RL Oncogene 15:1363-1367(1997).  
DR EMBL; Y10258; CAA71308.1; -.  
DR HSP; P04637; 1YCS.  
DR PFAM; PFO0870; P53; 1.  
DR NON\_TER 1  
SQ SEQUENCE 634 AA; 71360 MW; D45E080D CRC32;

Query Match 52.5%; Score 1777; DB 11; Length 634;  
Best Local Similarity 55.3%; Pred. No. 2.5e-134;  
Matches 361; Conservative 92; Mismatches 144; Indels 56; Gaps 17;

QY 8 SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNVVGTTSSMDVHLEGMTT 59  
DB 5 SPE---VFGHWDLEQICSVQPIDLNFVDEPSENATNKI-----EISMDCTRQMSDL 57  
QY 60 S-----VMAQFNLLSTMDQSSRAASAPYTPHAA-SVTPHSPYAPQSTFTDMSAP 113  
DB 58 SDPMWQYTNLGLLNMDOQIQNGSSSTPYNTDHAQNSVAPSPYAPQSTFDALSPSP 117  
QY 114 VPSNTDYPGPHFEVTFQOSSTAKSATWYSPLLKLYCOIATCPIQIKVSTPPPGT 173  
DB 118 AIPSNTDYPGPHSFVDFQOSSTAKSATWYSTELKLYCOIATCPIQIKVSTPPQGA 177  
QY 174 AIRAMPVYKAEHVDVVKRCNPNHSLGRDFNEGOSAPASHLIRVEGNLQYVDDPVTR 233  
DB 178 VIRAMPVYKAEHVEVVKRCNPNHSLREFNEGQIAPPASHLIRVEGNHQAQYVEDPITR 237  
QY 234 QSVVYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDGQVLRGRSFEGR 293  
DB 238 QSVLYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDGQVLRGRCFEAR 297  
QY 294 ICACGRDKADEHYREQQALNESSAKRAKQSPVAPALGAGVKKRRRGGED 353  
DB 298 ICACGRDKADEHSIRKQV--SDSAKNGDGTFRPQNTHTGQM--TSIKRRSPDDE 353  
QY 354 TYLVQVRENFELMKLESLELMELVQPLVDVSYRQOQO-----LLQRPHLQ-PPSY 407  
DB 354 LLYLVQVRENYEMLLKIKESLELMQYLPQHTIETIRQOQOQHLLQKQTSISQSSY 413  
QY 408 GPVLSPMKNVHGMMKLPVNLQYQPPHSSAATNLGPVGPQ---MLNNGHAPVAN 463  
DB 414 GNSPPLKNN--SMKLPVSQLIN--PQNNALTPPTPDGMGANTPMGTH--MPMA 467  
QY 464 GEMSSSSSAQ-----SMVSGSHCTPPPPYHADPSLYSLTGLGCPNCIEYFTSOGLQSI 517  
DB 468 GDMGLSPTQALPPPLSPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLT 527  
QY 518 YHLQNTLEDIGALKIPEQYRMTWRGLQDLKQGHYSTAQQLRS--SNATISIGSGSE 576  
DB 528 YQIHYSDMLASLKIPEQFRHAIWKGLDRLHQLRHEFSFSPHLPSPGASTVSV--GSSE 586  
QY 577 LQQRVMEAVHFRVHTITIPNRGPGGPPDEWADFGLDPCCKARKQIKEE 629  
DB 587 TRGERVIDAVRFTLRQITISFPFR-----DEWDFNDFMDARRNQORKEE 632

RESULT 9  
O89097

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O89097 PRELIMINARY; PRT; 586 AA.
O89097;
01-NOV-1998 (TREMELrel. 08, Created)
01-NOV-1998 (TREMELrel. 08, Last sequence update)
01-NOV-1999 (TREMELrel. 12, Last annotation update)
DN P63 ALPHA.
P73H.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
MEDLINE: 98448095.
YANG A., KAGHAD M., GILLET E., FLEMING M.D., DOTSCH V., ANDREWS N.C.,
CAPUT D., MCKEON F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities."
Mol. Cell 2:305-316(1998).
[2]
SEQUENCE FROM N.A.
TISSUE=THYMUS.
MEDLINE: 98369596.
SENOO M., SEKI N., OHIRA M., SUGANO S., WATANABE M., TACHIBANA M.,
TANAKA T., SHINKAI Y., KATO H.;
"A second p53-related protein, p73L, with high homology to p73."
Biochem. Biophys. Res. Commun. 248:603-607(1998).
EMBL: AF075439; AAC62644.1; -.
EMBL: AB010152; BAA32432.1; -.
HSP: P04637; LYCS.
PFAM: PF00870; P53.1.
PRINTS: PR00386; P53SUPPRESSR.
SEQUENCE 586 AA; 65789 MW; 2C644135 CRC32;

Query Match 51.58; Score 1743; DB 11; Length 586;
Best Local Similarity 59.78; Pred. No. 1.2e-131;
Matches 347; Conservative 8; Mismatches 116; Indels 36; Gaps 13;

67 LLSTMDQSSRAASASPTPEHAA-SVPTSPYAPQSSFTDMSAPVIPSNTDYPGP 125
22 LLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDMSAPVIPSNTDYPGP 81
126 HEFTVQOOSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKAE 185
82 SDVSFQOOSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKAE 141
186 HYTVVYKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPVTGROSVVVYEP 245
142 HYTVVYKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPVTGROSVVVYEP 201
246 GTEFTTILYFNCNCSVCGMNRRLIITILEMRDQVLRGRSFEGRICACPGDRKAD 305
202 GTEFTTILYFNCNCSVCGMNRRLIITILEMRDQVLRGRSFEGRICACPGDRKAD 261
306 EDHYREQQALNFSNAKGAASRAFKQSPAPVAPALGACVKKRRHGDDETYLQVGR 365
262 EDSIRKQV--SDSIRKQV--SDSIRKQV--SDSIRKQV--SDSIRKQV--SDSIRKQV 317
366 EILMKLKSLELMELVQPLVDVSYRQOQO-----LLQRPShLQ-PPSYGVLSPMKNVHG 419
318 EMLLKESLELMELVQPLVDVSYRQOQO-----LLQRPShLQ-PPSYGVLSPMKNVHG 377
420 GNNKLPVNLVGVGPPHSSAATPNLGPVGP-----MLNNGHGVAPANGEMSSSHSAQ-- 474
377 SNKLPVSVQLIN--PQORNALTPPTPEGMANGNIPMGTH---MPMANGDNGLSPTQAL 431
474 ----SNVSGSHTPPPPYHADPSLVSLFTGLGCPNCIEYFTSQGLSIYHLQNTIEDLG 529
432 PPLSLMPSTSHCTPPPPYPTDCSIVSFLARLQSSCLDYFTTQGLTTIYQIEHNSMDLA 491
530 ALKIPQYRMTWIRGLQDLKQGHYSTAQQLRS-SNAATISIGSGELQQRVMEAVHF 588
492 SLKIPQYRMTWIRGLQDLKQGHYSTAQQLRS-SNAATISIGSGELQQRVMEAVHF 550
589 RVRHTTIPNRGCGGPGDEWADFQDLPDCKARKQPIKEE 629
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Db 551 TLRQTSFPFR-----DEWNEFMDARRNQORKEE 584

**RESULT 11**

075078	PRELIMINARY;	PRT; 448 AA.
ID 076078		
AC 076078;		
DT 01-NOV-1998	(TREMBLrel. 08, Created)	
DT 01-NOV-1998	(TREMBLrel. 08, Last sequence update)	
DT 01-NOV-1999	(TREMBLrel. 12, Last annotation update)	
DE TA P63 GAMMA.		

OS Homo sapiens (human).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RC [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE: 98448095.  
 RA YANG A., KAGHAN M., GILLET E., FLEMING M.D., DOTSCH V., ANDREWS N.C.,  
 RA CAPUT D., MCKEON F.;  
 RA "p63, a p53 homolog at 3q27-29, encodes multiple products with  
 RT transactivating, death-inducing, and dominant-negative activities.";  
 RL Mol. Cell 2:305-316(1998).  
 RL [2]

Query Match 38.3%; Score 1297.5; DB 4; Length 448;  
Best Local Similarity 61.4%; Pred. No. 4.le-96;

[illegible]

**RESULT** 12

Q88897	PRELIMINARY; PRPT; 483 AA.
ID	Q88897
AC	Q88897;
DT	01-NOV-1998 (TREMBlrel. 08, Created)
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT	01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE	TA*P63 GAMMA.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
FX	MEDLINE; 98448095.
RA	YANG A., KAGHAD M., GILLETTE E., FLEMING M.D., DOTSCH V., ANDREWS N.C.,
RA	CAPUT D., MCKEON F.;
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with
RT	transactivating, death-inducing, and dominant-negative activities.";
EL	Mol. Cell 2:305-316(1998).
EL	EMBL; AF073434; AAC62639.1; -.
DR	HSSP; P04637; LYCS.
DR	PFAM; PF00870; P53; 1.
DR	PRINTS; PRO0386; P53SUPPRESSR.
SO	SEQUENCE 483 AA; 54969 MW; 4AF2A2C4 CRC32;

Query Match 38.0%; Score 1284.5; DB 11; Length 483;  
Best Local Similarity 56.7%; Pred. No. 5e-95;  
Matches 267; Conservative 50; Mismatches 91; Indels 63; Gaps 13;

[illegible]

RESULT 13

ID	PRELIMINARY;	PRT;	393 AA.
075922			
AC	075922;		
DT	01-NOV-1998 (TREMRel. 08, Created)		
DT	01-NOV-1998 (TREMRel. 08, Last sequence update)		
DT	01-NOV-1999 (TREMRel. 12, Last annotation update)		
DE	DN P63 GAMMA.		
OS	DS Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.		



[1] SEQUENCE FROM N.A.  
MEDLINE; 98448095.  
YANG A., KAGHAD M., GILLET E., FLEMING M.D., DOTSCH V., ANDREWS N.C.,  
CAPUT D., MCKEON F.;  
"p53, a p53 homolog at 3q27-29, encodes multiple products with  
transactivating, death-inducing, and dominant-negative activities.";  
Mol. Cell 2:305-316(1998).  
EMBL; AF075429; AAC62634.1; -.  
HSSP; P04637; LYCS.  
PFAM; PF00870; P53; 1.  
PRINTS; PR00386; P53SUPPRESSOR.  
SEQUENCE 393 AA; 44658 MW;  
168F96F6 CRC32;

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ery Match          36.9%; Score 1248.5; DB 4; Length 393;
at Local Similarity 70.6%; Pred. No. 2.9e-92;
ches 238; Conservative 37; Mismatches 55; Indels 7; Gaps
67  LLSTMDQMSRAASASPYTPEAA--SVPHSPYAPQSSFTETMSPAPVIPNTDYPGPH 125
   ||| ||| : : : ||| ||| ||| ||| ||| ||| : ||| ||| ||| |||
22  LNSMDQIQNGSSSTGYWTDRAQNSVATPSPYAPQSSFTDALSPSPAINSTDYPGPH 81
   ||| ||| : : : ||| ||| ||| ||| ||| ||| : ||| ||| ||| |||
126 HFEVTFQOSTAKSATWYSPLKUKLYCQIAKTCPTQIKVSTPPPPGFAIRAMPYKKA 185
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
82  SFDVSFQOSTAKSATWYSTELKUKLYCQIAKTCPTQIKVMPPPGQAVIRAMPYKKA 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
136 HVTDVVKRCPNHLEGRDFNGSQAPASHLIRVEGNLSOYDDVDTGVSQSVVVPYEPQV 245
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
142 HVTDVVKRCPNHLSREFNEGQIAPPSSLIRIVBEGNSHAQYVEDPTIGRQSLVLPYEPQV 201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
246 GTEFTTLYNFMNCSSCGGMNRRPILITILEMRDGOVLGRSFEGRICACPGDRKAD 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
202 GTEFTTLYNFMNCSSCGGMNRRPILIVLETRGOVLGRCFEARICACPGDRKAD 261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
306 EDHYREQOALNESSAKNGAASKRAFQKSPAPVAPALGAGVKKRRHGDEDTYTLQVGRNF 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
262 EDSIRKQOV--SDSTKNGDCTKPRFRQNTHQIM--TSJKRRSPDDELLIYLVGRETY 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
356 EILMKRESLELMELVDPQLVDYSYRQOQLLQRPSHL 402
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
318 EMLLKRESLELMOYLPOHTIETRYQOQO--QQHQHL 352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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.T 14  
 99  
 O88899 PRELIMINARY: PRT; 389 AA.  
 O88899; O88899  
 01-NOV-1998 (T-EMBLrel. 08, Created)  
 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)  
 01-NOV-1999 (T-EMBLrel. 12, Last annotation update)  
 DN P63 GAMMA.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE; 98448095.  
 YANG A.; KAGHAD M.; GILLET E.; FLEMING M.D.; DOTSCH V.; ANDREWS N.C.;  
 CAPUT D.; MCKEON F.;  
 "p63, a p53 homolog at 3q27-29, encodes multiple products with  
 transactivating, death-inducing, and dominant-negative activities.";  
 Mol. Cell 2:305-316(1998).  
 EMBL; AF075437; AAC62642.1; -.  
 HSPB; P04637; IYCS.  
 PFAM; PF00870; P53; 1.  
 PRINTS; PR00386; P53SUPPRESSOR.  
 SEQUENCE 389 AA; 43970 MW; C054EEDA CRC32;

Every Match 36.6%; Score 1238.5; DB 11; Length 389;  
 t Local Similarity 63.9%; Pred. NO. 1.8e-91;  
 Mismatches 248; Conservative 38; Mismatches 63; Indels 39; Gaps

QY	67	LLSSTWDQKSRRAASAPYTPTEHAA-SVPTHSPYAQPSTSTDTMSPAPVIPSNTDYPGPH	125
Db	22	LLNSMDQIQGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSTNDYPGPH	81
QY	126	HEEVTFOQSSAKSATYTSPLKLKLYCOIAKTCPIQIKVSTPPPCFATRAMPVYKKA	185
Db	82	SDVTSFQSSAKSATYTSPLKLKLYCOIAKTCPIQIKVSTPPPCFATRAMPVYKKA	141
QY	186	HYTDVVKPCPNHELGRDFNEGQSPASHLIRVEGNLKSQYVDDPVTGRQSVVYPPYPPQV	245
Db	142	HVTEVVKPCPNHELGRDFNEGQSPASHLIRVEGNLKSQYVDDPVTGRQSVVYPPYPPQV	201
QY	246	GTEFTILYNFMCNSSCVGMNRRPILIIITILEMDGQVGLRRSFEGRICACGRDKAD	305
Db	202	GTEFTILYNFMCNSSCVGMNRRPILIIITILEMDGQVGLRRSFEGRICACGRDKAD	261
QY	306	EDRYEQALNESAANKAAKRAFKQSPYAPALGACVKKRRHGDEDTYYLQVGRGNF	365
Db	262	EDSIRKQV---SDSAKNG---DAFRONTHGIOM--TSIKKRRSPDDDELLYLPVGRREY	313
QY	366	ELMLKESLEMLVQPLVDYSYRQQQ-----LLQRPSSL-----OPPSYGPV	410
Db	314	EMLKAKESLEMLVQPLVDYSYRQQQ-----LLQRPSSL-----OPPSYGPV	371
QY	411	LSPMKNVHGGMKLPVSNQLVGQPPPHS	438
Db	372	QSDVFEFR-----SNPPNHS	386
RESULT 15			
Q27937			
AC	Q27937	PRELIMINARY;	PRT; 564 AA.
ID	Q27937;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DE	P53 TUMOR SUPPRESSOR HOMOLOG.		
GN	GN SQP53.		
OC	Loligo forbesi (Northern European squid).		
OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;		
OC	Myopsida; Loliginidae; Loligo.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OPTIC LOBE;		
RA	WINGE P., FRIEND S., FLEMING J.T.;		
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; U43595; AAA8563.1; -		
DR	EMBL; U43596; AAA98564.1; -		
DR	HSP; P04637; ITSR.		
DR	PFAM; PF00870; P53; 1.		
DR	PRINTS; PR00386; P53SUPPRESSOR.		
SQ	SEQUENCE 564 AA; FCE61653 CRC32;		

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Query Match      25.4%; Score 859.5; DB 5; Length 564;
Best Local Similarity 33.3%; Pred. NO. 6.8e-61;
Matches 214; Conservative 96; Mismatches 200; Indels 133; Gaps 18;

QY      4  STATPDGGTTFEHLWSL-----EPDSTVFDLPQSSRGNNE 40
Db      1  : : : : : : : : : : : : : : : : : : : : : :
Db      2  SQGTSFNSQETFNLLWDSLEQVTANEYQIHERGVGYEYEAEPDQTSLEISAYRIAQPD 61
QY      41  VVGGTDSMDVFHLEGHTTSTVMAQFNLLSTMDQSSRAASAPYTPHEAASVPYHSPY- 100
Db      1  : : : : : : : : : : : : : : : : : : : : : :
Db      62  PYGRSES-----YDLNPIINQI-----PAPMPIADTQNPLVNVHCPE 100
QY      100  -----AQPSSTFD-TMSPAPVIGNTDYPGPHFEVTF-QQSSTAKSATWYSPPLKKLY 152
Db      101  EMPVSTYSPSHDVQSPQSPVPSNIKYGPYFENFSFAQPSKETKSTWTYSEKLDKLY 160
QY      153  COIAKTCPIQIKVSTPPPPPTATRAMPVYKKAESHVDVVKRCNPHELGDRNEGOSAPAS 212
Db      1  : : : : : : : : : : : : : : : : : : : : : :

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